

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 16:38:57 ; Search time 1672 Seconds
(without alignments)
434.706 Million cell updates/sec

Title: US-09-825-482-6

Perfect score: 15

Sequence: 1 agataccacacgcag 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1437254

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 15 | 100.0 | 15 | 6 | AX352370 Sequence |
| 2 | 15 | 100.0 | 17 | 6 | AX352371 Sequence |
| 3 | 15 | 100.0 | 22 | 6 | AX352373 Sequence |
| 4 | 15 | 100.0 | 25 | 6 | I22533 Sequence 21 |
| 5 | 15 | 100.0 | 25 | 6 | I47358 Sequence 21 |
| 6 | 14.6 | 97.3 | 25 | 6 | I14212 Sequence 9 |
| 7 | 14.6 | 97.3 | 25 | 6 | I22540 Sequence 28 |
| 8 | 14.6 | 97.3 | 25 | 6 | I47365 Sequence 28 |
| 9 | 13.4 | 89.3 | 25 | 6 | I22538 Sequence 26 |
| 10 | 13.4 | 89.3 | 25 | 6 | I22783 Sequence 27 |
| 11 | 13.4 | 89.3 | 25 | 6 | I47363 Sequence 26 |
| 12 | 13.4 | 89.3 | 25 | 6 | I47608 Sequence 27 |
| 13 | 13 | 86.7 | 21 | 6 | I12777 Sequence 75 |
| 14 | 13 | 86.7 | 22 | 6 | I12778 Sequence 76 |
| 15 | 12.4 | 82.7 | 14 | 6 | AX352367 Sequence |
| 16 | 12.4 | 82.7 | 20 | 6 | AX063311 Sequence |
| 17 | 12.4 | 82.7 | 25 | 6 | AR095910 Sequence |
| 18 | 12.4 | 82.7 | 25 | 6 | I22618 Sequence 10 |
| 19 | 12.4 | 82.7 | 25 | 6 | I47443 Sequence 10 |

| | | | | | | |
|---|----|------|------|----|---|--------------------|
| c | 20 | 12.4 | 82.7 | 27 | 6 | AR095909 Sequence |
| | 21 | 11.8 | 78.7 | 15 | 6 | AX352372 Sequence |
| | 22 | 11.8 | 78.7 | 25 | 6 | I22534 Sequence 22 |
| | 23 | 11.8 | 78.7 | 25 | 6 | I47359 Sequence 22 |
| c | 24 | 11.4 | 76.0 | 18 | 6 | BD089434 A method |
| | 25 | 11.4 | 76.0 | 24 | 6 | AR349788 Sequence |
| | 26 | 11.4 | 76.0 | 30 | 6 | A21743 oligonucleo |
| | 27 | 11 | 73.3 | 20 | 6 | BD177288 Sulfotran |
| | 28 | 11 | 73.3 | 20 | 6 | AX615193 Sequence |
| | 29 | 11 | 73.3 | 20 | 6 | AX643840 Sequence |
| | 30 | 11 | 73.3 | 21 | 6 | AX119403 Sequence |
| | 31 | 11 | 73.3 | 29 | 6 | BD182768 Novel (R) |
| | 32 | 11 | 73.3 | 29 | 6 | AX616507 Sequence |
| | 33 | 10.8 | 72.0 | 14 | 6 | AX352366 Sequence |
| c | 34 | 10.8 | 72.0 | 18 | 6 | BD093685 Human lp3 |
| c | 35 | 10.8 | 72.0 | 20 | 6 | AR316227 Sequence |
| c | 36 | 10.8 | 72.0 | 20 | 6 | AR409583 Sequence |
| | 37 | 10.8 | 72.0 | 20 | 6 | AX231599 Sequence |
| | 38 | 10.8 | 72.0 | 20 | 6 | AX231709 Sequence |
| | 39 | 10.8 | 72.0 | 23 | 6 | BD143029 Method of |
| c | 40 | 10.8 | 72.0 | 24 | 6 | E24994 Apoptosis-1 |
| c | 41 | 10.8 | 72.0 | 24 | 6 | AR397558 Sequence |
| | 42 | 10.8 | 72.0 | 24 | 6 | AX443853 Sequence |
| c | 43 | 10.8 | 72.0 | 25 | 6 | AX375203 Sequence |
| | 44 | 10.8 | 72.0 | 25 | 6 | AX447831 Sequence |
| | 45 | 10.8 | 72.0 | 26 | 6 | AR091105 Sequence |

ALIGNMENTS

| | | | | | | |
|------------|---|-------------|-------|-----|--------|-----------------|
| RESULT 1 | AX352370 | AX352370 | 15 bp | DNA | linear | PAT 06-FEB-2002 |
| LOCUS | Sequence 6 from Patent WO0175174. | | | | | |
| DEFINITION | AX352370 | | | | | |
| ACCESSION | AX352370.1 | GI:18617644 | | | | |
| VERSION | | | | | | |
| KEYWORDS | synthetic construct | | | | | |
| SOURCE | other sequences; artificial sequences. | | | | | |
| ORGANISM | | | | | | |
| REFERENCE | 1 | | | | | |
| AUTHORS | Cohenford, M.A. and Lentricchia, B. | | | | | |
| TITLE | Detection and typing of human papillomavirus using pna probes | | | | | |
| JOURNAL | Patent: WO 0175174-A 6 11-OCT-2001; | | | | | |
| | CYTIC CORPORATION (US) | | | | | |
| FEATURES | Location/Qualifiers | | | | | |
| source | 1..15 | | | | | |
| | /organism="synthetic construct" | | | | | |
| | /mol_type="unassigned DNA" | | | | | |
| | /db_xref="taxon:32630" | | | | | |
| | /note="PNA Probe VI" | | | | | |

| | | | | | |
|------------|--|-----------------|--------------------|-------|---------------|
| ORIGIN | Query Match | 100.0%; | Score 15; | DB 6; | Length 15; |
| | Best Local Similarity | 100.0%; | Pred. No. 2.7e+02; | | |
| | Matches | 15; | Conservative | 0; | Mismatches 0; |
| | | | | | Indels 0; |
| | | | | | Gaps 0; |
| Qy | 1 | AGATACCACACGCAG | 15 | | |
| | | | | | |
| Db | 1 | AGATACCACACGCAG | 15 | | |
| | | | | | |
| RESULT 2 | AX352371 | AX352371 | 17 bp | DNA | linear |
| LOCUS | Sequence 7 from Patent WO0175174. | | | | |
| DEFINITION | AX352371 | | | | |
| ACCESSION | AX352371.1 | GI:18617645 | | | |
| VERSION | | | | | |
| KEYWORDS | synthetic construct | | | | |
| SOURCE | synthetic construct | | | | |
| ORGANISM | other sequences; artificial sequences. | | | | |

REFERENCE 1
AUTHORS Cohenford, M.A. and Lentrichia, B.
TITLE Detection and typing of human papillomavirus using pna probes
JOURNAL Patent: WO 0175174-A 7 11-OCT-2001;
CYTYC CORPORATION (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PNA Probe VII"

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15
|||||
Db 2 AGATACCACACGCAG 16

RESULT 3
AX352373
LOCUS AX352373 22 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 9 from Patent WO0175174.
ACCESSION AX352373
VERSION AX352373.1 GI:18617647
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Cohenford, M.A. and Lentrichia, B.
TITLE Detection and typing of human papillomavirus using pna probes
JOURNAL Patent: WO 0175174-A 9 11-OCT-2001;
CYTYC CORPORATION (US)
FEATURES Location/Qualifiers
source 1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="MC01 HPV consensus primer sequence"

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15
|||||
Db 7 AGATACCACACGCAG 21

RESULT 4
I22533
LOCUS I22533 25 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 21 from patent US 5527898.
ACCESSION I22533
VERSION I22533.1 GI:1602887
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer, H.M., Gravitt, P.E., Greer, C.E., Manos, M. Michele.,
Reanick, R.M. and Zhang, T.Y.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5527898-A 21 18-JUN-1996;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 97.3%; Score 14.6; DB 6; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15
|||||
Db 8 AGATACCACACGCAG 22

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15
|||||
Db 8 AGATACCACACGCAG 22

RESULT 5
I47358
LOCUS I47358 25 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 21 from patent US 5639871.
ACCESSION I47358
VERSION I47358.1 GI:2471323
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer, H.M., Gravitt, P.E., Greer, C.E., Impraim, C.C.,
Manos, M. Michele., Resnick, R.M. and Zhang, T.Y.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5639871-A 21 17-JUN-1997;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15
|||||
Db 8 AGATACCACACGCAG 22

RESULT 6
I14212
LOCUS I14212 25 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 9 from patent US 5447839.
ACCESSION I14212
VERSION I14212.1 GI:997227
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Manos, M. Michele., Bauer, H.M., Greer, C.E., Resnick, R.M. and Ting, Y.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5447839-A 9 05-SEP-1995;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 97.3%; Score 14.6; DB 6; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15
|||||
Db 8 AGATACCACACGCAG 22

RESULT 7
I22540
LOCUS I22540 25 bp DNA linear PAT 07-OCT-1996

DEFINITION Sequence 28 from patent US 5527898.
ACCESSION I22540
VERSION I22540.1 GI:1602894
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
Resnick,R.M. and Zhang,T.Y.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5527898-A 28 18-JUN-1996;
FEATURES Location/Qualifiers
source
1. .25
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 97.3%; Score 14.6; DB 6; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGATACCACACGCAG 15
Db 8 AGATACCACACGCAG 22
|||||:|||||
RESULT 8
LOCUS I47365 25 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 28 from patent US 5639871.
ACCESSION I47365
VERSION I47365.1 GI:2471330
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Impraim,C.C.,
Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5639871-A 28 17-JUN-1997;
FEATURES Location/Qualifiers
source
1. .25
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 97.3%; Score 14.6; DB 6; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGATACCACACGCAG 15
Db 8 AGATACCACACGCAG 22
|||||:|||||
RESULT 9
LOCUS I22538 25 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 26 from patent US 5527898.
ACCESSION I22538
VERSION I22538.1 GI:1602892
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
Resnick,R.M. and Zhang,T.Y.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5527898-A 26 18-JUN-1996;
FEATURES Location/Qualifiers

source 1. .25
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 89.3%; Score 13.4; DB 6; Length 25;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AGATACCACACGCAG 15
Db 8 AGATACCACACGCAG 22
|||||:|||||
RESULT 10
LOCUS I22783 25 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 271 from patent US 5527898.
ACCESSION I22783
VERSION I22783.1 GI:1603137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
Resnick,R.M. and Zhang,T.Y.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5527898-A 271 18-JUN-1996;
FEATURES Location/Qualifiers
source
1. .25
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 89.3%; Score 13.4; DB 6; Length 25;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AGATACCACACGCAG 15
Db 8 AGATACCACACGCAG 22
|||||:|||||
RESULT 11
LOCUS I47363 25 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 26 from patent US 5639871.
ACCESSION I47363
VERSION I47363.1 GI:2471328
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Impraim,C.C.,
Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5639871-A 26 17-JUN-1997;
FEATURES Location/Qualifiers
source
1. .25
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 89.3%; Score 13.4; DB 6; Length 25;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AGATACCACACGCAG 15
Db 8 AGATACCACACGCAG 22
|||||:|||||

```
RESULT 12
LOCUS      I47608
DEFINITION Sequence 271 from patent US 5639871.
ACCESSION  I47608
VERSION     I47608.1 GI:2471573
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Bauer,H.M., Gravitte,P.B., Greer,C.E., Impraim,C.C.,
            Manos,M.Michele, Resnick,R.M. and Zhang,T.Yi.
TITLE       Detection of human papillomavirus by the polymerase chain reaction
JOURNAL     Patent: US 5639871-A 271 17-JUN-1997;
FEATURES    Location/Qualifiers
            source          1..25
                        /organism="unknown"
                        /mol_type="unassigned DNA"
ORIGIN
Query Match      89.3%; Score 13.4; DB 6; Length 25;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AGATACCACACGCAG 15
Db      8 AGATACCACACGCAG 22
      |||||
      |||||

RESULT 13
LOCUS      I12777
DEFINITION Sequence 75 from patent US 5427930.
ACCESSION  I12777
VERSION     I12777.1 GI:910159
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Birkenmeyer,L.G., Carrino,J.J., Dille,B.J., Hu,H.-Y.,
            Kratochvil,J.D., Laffler,T.G., Marshall,R.L., Rinehardt,L.A. and
            Solomon,N.A.
TITLE       Amplification of target nucleic acids using gap filling ligase
JOURNAL     Patent: US 5427930-A 75 27-JUN-1995;
FEATURES    Location/Qualifiers
            source          1..21
                        /organism="unknown"
                        /mol_type="unassigned DNA"
ORIGIN
Query Match      86.7%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GATACCACACGCA 14
Db      9 GATACCACACGCA 21
      |||||
      |||||

RESULT 14
LOCUS      I12778/c
DEFINITION Sequence 76 from patent US 5427930.
ACCESSION  I12778
VERSION     I12778.1 GI:910160
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 22)
AUTHORS     Birkenmeyer,L.G., Carrino,J.J., Dille,B.J., Hu,H.-Y.,
            Kratochvil,J.D., Laffler,T.G., Marshall,R.L., Rinehardt,L.A. and
            Solomon,N.A.
TITLE       Amplification of target nucleic acids using gap filling ligase
JOURNAL     Patent: US 5427930-A 76 27-JUN-1995;
FEATURES    Location/Qualifiers
            source          1..22
                        /organism="unknown"
                        /mol_type="unassigned DNA"
ORIGIN
Query Match      86.7%; Score 13; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GATACCACACGCA 15
Db      1 GATACCACACGCA 14
      |||||
      |||||

Search completed: June 23, 2005, 18:52:40
Job time : 1675 secs
```

```
REFERENCE   1 (bases 1 to 22)
AUTHORS     Birkenmeyer,L.G., Carrino,J.J., Dille,B.J., Hu,H.-Y.,
            Kratochvil,J.D., Laffler,T.G., Marshall,R.L., Rinehardt,L.A. and
            Solomon,N.A.
TITLE       Amplification of target nucleic acids using gap filling ligase
JOURNAL     Patent: US 5427930-A 76 27-JUN-1995;
FEATURES    Location/Qualifiers
            source          1..22
                        /organism="unknown"
                        /mol_type="unassigned DNA"
ORIGIN
Query Match      86.7%; Score 13; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GATACCACACGCA 14
Db      13 GATACCACACGCA 1
      |||||
      |||||

RESULT 15
LOCUS      AX352367
DEFINITION Sequence 3 from Patent WO0175174.
ACCESSION  AX352367
VERSION     AX352367.1 GI:18617641
KEYWORDS    synthetic construct
            other sequences; artificial sequences.
ORGANISM
REFERENCE   1
AUTHORS     Cohenford,M.A. and Lentrichia,B.
TITLE       Detection and typing of human papillomavirus using pna probes
JOURNAL     Patent: WO 0175174-A 3 11-OCT-2001;
            CVTVC CORPORATION (US)
FEATURES    Location/Qualifiers
            source          1..14
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="PNA Probe III"
ORIGIN
Query Match      82.7%; Score 12.4; DB 6; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GATACCACACGCAG 15
Db      1 GATACCACACGCAG 14
      |||||
      |||||

Search completed: June 23, 2005, 18:52:40
Job time : 1675 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 16:28:51 ; Search time 418 Seconds
(without alignments)
212.431 Million cell updates/sec

Title: US-09-825-482-6

Perfect score: 15

Sequence: 1 agataccacacgcag 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 3522762

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 15 | 100.0 | 15 | 5 | Aai70567 Human pap |
| 2 | 15 | 100.0 | 15 | 12 | ADO08491 |
| 3 | 15 | 100.0 | 17 | 5 | Aai70568 Human pap |
| 4 | 15 | 100.0 | 17 | 12 | ADO08492 |
| 5 | 15 | 100.0 | 22 | 5 | Aai70570 Human pap |
| 6 | 15 | 100.0 | 22 | 12 | ADO08494 |
| 7 | 15 | 100.0 | 25 | 2 | AAQ56371 L1 consen |
| 8 | 15 | 100.0 | 25 | 2 | AAQ56337 Genital H |
| 9 | 15 | 100.0 | 25 | 2 | AAT44733 L1 consen |
| 10 | 15 | 100.0 | 25 | 2 | AAT77886 Human pap |
| 11 | 15 | 100.0 | 25 | 2 | Aavi7472 Primer FS |
| 12 | 15 | 100.0 | 26 | 2 | AAG87034 Oligonucl |
| 13 | 14.6 | 97.3 | 25 | 2 | AAT10813 Human pap |
| 14 | 14.6 | 97.3 | 25 | 2 | AAT44761 L1 consen |
| 15 | 14.6 | 97.3 | 25 | 2 | AAT77893 Human pap |
| 16 | 14.6 | 97.3 | 25 | 2 | Aavi7427 Probe MY4 |
| 17 | 13.4 | 89.3 | 25 | 2 | AAQ56373 L1 consen |
| 18 | 13.4 | 89.3 | 25 | 2 | AAT10814 Human pap |
| 19 | 13.4 | 89.3 | 25 | 2 | AAT44759 L1 consen |
| 20 | 13.4 | 89.3 | 25 | 2 | AAT44906 L1 consen |

| | | | | | | |
|------|------|------|----|----|----------|--------------------|
| 21 | 13.4 | 89.3 | 25 | 2 | AAT78135 | Aat78135 Human pap |
| 22 | 13.4 | 89.3 | 25 | 2 | AAQ77891 | Aat77891 Human pap |
| 23 | 13 | 86.7 | 21 | 2 | AAQ36079 | Aaq36079 HPV detec |
| c 24 | 13 | 86.7 | 22 | 2 | AAQ36080 | Aaq36080 HPV detec |
| c 25 | 13 | 86.7 | 29 | 5 | Aaf61731 | Aaf61731 E. coli C |
| c 26 | 13 | 86.7 | 29 | 5 | Aaf61734 | Aaf61734 E. coli C |
| c 27 | 12.6 | 84.0 | 29 | 5 | AAQ61730 | Aaf61730 E. coli C |
| 28 | 12.4 | 82.7 | 14 | 5 | AAI70564 | Aai70564 Human pap |
| 29 | 12.4 | 82.7 | 14 | 12 | ADO08473 | Ado08473 Human pap |
| 30 | 12.4 | 82.7 | 20 | 2 | AZ30418 | Aaz30418 Wheat MLO |
| 31 | 12.4 | 82.7 | 20 | 4 | Aaf24619 | Aaf24619 PCR prime |
| 32 | 12.4 | 82.7 | 20 | 4 | AAQ24592 | Aaf24592 PCR prime |
| 33 | 12.4 | 82.7 | 25 | 2 | AAQ56372 | Aaq56372 L1 consen |
| 34 | 12.4 | 82.7 | 25 | 2 | AAT10812 | Aat10812 Human pap |
| 35 | 12.4 | 82.7 | 25 | 2 | AAT44873 | Aat44873 HPV L1 co |
| 36 | 12.4 | 82.7 | 25 | 2 | AAT77970 | Aat77970 Human pap |
| 37 | 12.4 | 82.7 | 25 | 9 | ACI70339 | Aci70339 Human mic |
| c 38 | 12.4 | 82.7 | 27 | 3 | AZ35317 | Aaz35317 Oligonucl |
| 39 | 11.8 | 78.7 | 15 | 5 | AAI70569 | Aai70569 Human pap |
| 40 | 11.8 | 78.7 | 15 | 12 | ADO08493 | Ado08493 Human pap |
| 41 | 11.8 | 78.7 | 18 | 12 | ADO16577 | Ado16577 4 synthes |
| 42 | 11.8 | 78.7 | 20 | 1 | AAQ90871 | Aan90871 Promoter |
| 43 | 11.8 | 78.7 | 20 | 12 | ADH72332 | Adh72332 Human for |
| 44 | 11.8 | 78.7 | 20 | 13 | ADR32107 | Adr32107 Hepatitis |
| 45 | 11.8 | 78.7 | 20 | 13 | ADR67797 | Adr67797 Hepatitis |

ALIGNMENTS

RESULT 1

AAI70567
ID AAI70567 standard; DNA; 15 BP.

XX AAI70567;

XX 21-JAN-2002 (first entry)

XX Human papillomavirus blocking probe VI.

XX HPV; probe; detection; typing; diagnosis; endocervical carcinoma;
KW cervical cancer; neoplasia; probe; ss.

XX Human papillomavirus.

PN W0200175174-A2.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010795.

XX 03-APR-2000; 2000US-0194304P.

XX 15-AUG-2000; 2000US-0225524P.

XX (CVTY-) CYTYC CORP.

XX Cohenford MA, Lentricchia B;

XX WPI; 2001-648563/74.

XX Detecting the presence of at least one selected strain of a disease
PT organism or of a target nucleic acid of a human papilloma virus in a
sample, comprises employing peptide-nucleic acid probes.

XX Claim 14; Page 24; 27pp; English.

XX The present sequence is that of nucleic acid probe VI, useful in the
detection of human papillomavirus (HPV) nucleic acids. The probe is
complementary to a portion of low-risk HPV strains 6 and 11, and binds to
a portion between the binding sites for primer set MY09/MY11 (see
AAI70571-72). The probe is used as a blocking probe to prevent
amplification of nucleic acids from low-risk HPV strains while nucleic
acids from high-risk strains to which the probe does not bind are

CC amplified by MY09/MY11. The method allows the specific detection of high-risk HPV nucleic acids and can be used to screen patient samples, e.g. cervical scrapings, for the presence of a high-risk HPV variant, especially type 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68 and 70. The presence of a particular target nucleic acid in sample cells is diagnostic of HPV infection, and may be indicative of risks of cancer, such as endocervical carcinoma, cervical cancer and neoplasia

XX Sequence 15 BP; 6 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15

Db 1 AGATACCACACGCAG 15

RESULT 2

ADO08491
ID ADO08491 standard; DNA; 15 BP.

XX ADO08491;

DT 12-AUG-2004 (first entry)

XX Human papillomavirus (HPV) detection-related PNA probe VI SeqID23.

DE detection; typing; Human Papilloma Virus; HPV; infection; PNA probe;
KW high-risk; infectious organism; probe; ss.

XX Human papillomavirus.

XX WO2004042071-A2.

XX 21-MAY-2004.

XX 07-OCT-2003; 2003WO-US031841.

XX 01-NOV-2002; 2002US-00286387.

XX (CYTY-) CYTYC CORP.

XX Cohenford MA, Lentricchia BB;

XX WPI; 2004-400683/37.

XX New peptide-nucleic acids, useful as a probe for detecting and typing Human Papilloma Virus infection, or in screening assay toward the diagnostically most-relevant strains or species of a disease organism.

XX Example 2; SEQ ID NO 23; 26pp; English.

XX This invention relates to a novel method for detection and typing of a Human Papilloma Virus (HPV) infection using PNA primers or probes, including methods for detecting high-risk types of HPV infection with minimal numbers of PNA probes or using PNA primers to selectively amplify only high-risk types of HPV. Specifically claimed are novel primer/probe sequences which are useful as primers/probes for detecting and typing HPV infection. The methods are used in a screening assay toward the diagnostically most-relevant strains or species of a disease organism or to selectively amplify high-risk strains of an infectious organism. The present sequence is that of a HPV PNA probe which was used in the exemplification of the invention.

XX Sequence 15 BP; 6 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15

Db 1 AGATACCACACGCAG 15

RESULT 3

AAI70568

ID AAI70568 standard; DNA; 17 BP.

XX AAI70568;

XX 21-JAN-2002 (first entry)

XX Human papillomavirus blocking probe VII.

XX HPV; probe; detection; typing; diagnosis; endocervical carcinoma;
KW cervical cancer; neoplasia; probe; ss.

XX Human papillomavirus.

XX WO200175174-A2.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010795.

XX 03-APR-2000; 2000US-0194304P.

XX 15-AUG-2000; 2000US-0225524P.

XX (CYTY-) CYTYC CORP.

XX Cohenford MA, Lentricchia B;

XX WPI; 2001-648563/74.

XX Detecting the presence of at least one selected strain of a disease organism or of a target nucleic acid of a human papilloma virus in a sample, comprises employing peptide-nucleic acid probes.

XX Claim 14; Page 25; 27pp; English.

XX The present sequence is that of nucleic acid probe VII, useful in the detection of human papillomavirus (HPV) nucleic acids. The probe is complementary to a portion of low-risk HPV strains 6 and 11, and binds to a portion between the binding sites for primer set MY09/MY11 (see AAI70571-72). The probe is used as a blocking probe to prevent amplification of nucleic acids from low-risk HPV strains while nucleic acids from high-risk strains to which the probe does not bind are amplified by MY09/MY11. The method allows the specific detection of high-risk HPV nucleic acids and can be used to screen patient samples, e.g. cervical scrapings, for the presence of a high-risk HPV variant, especially type 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68 and 70. The presence of a particular target nucleic acid in sample cells is diagnostic of HPV infection, and may be indicative of risks of cancer, such as endocervical carcinoma, cervical cancer and neoplasia

XX Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15

Db 2 AGATACCACACGCAG 16

RESULT 4

ADO08492
ID ADO08492 standard; DNA; 17 BP.

XX ADO08492;

XX 12-AUG-2004 (first entry)

XX DE Human papillomavirus (HPV) detection-related PNA probe VII SeqID24.
 XX KW detection; typing; Human Papilloma Virus; HPV; infection; PNA probe;
 XX KW high-risk; infectious organism; probe; ss.
 XX OS Human papillomavirus.
 XX PN WO2004042071-A2.
 XX PD 21-MAY-2004.
 XX PF 07-OCT-2003; 2003WO-US031841.
 XX PR 01-NOV-2002; 2002US-00286387.
 XX PA (CVTY-) CYTVC CORP.
 XX PI Cohenford MA, Lentricchia BB;
 XX DR WPI; 2004-400683/37.
 XX PT New peptide-nucleic acids, useful as a probe for detecting and typing
 XX PT Human Papilloma Virus infection, or in screening assay toward the
 XX PT diagnostically most-relevant strains or species of a disease organism.
 XX PS Example 2; SEQ ID NO 24; 26pp; English.
 XX SQ This invention relates to a novel method for detection and typing of a
 CC Human Papilloma Virus (HPV) infection using PNA primers or probes,
 CC including methods for detecting high-risk types of HPV infection with
 CC minimal numbers of PNA probes or using PNA primers to selectively amplify
 CC only high-risk types of HPV. Specifically claimed are novel primer/probe
 CC sequences which are useful as primers/probes for detecting and typing HPV
 CC infection. The methods are used in a screening assay toward the
 CC diagnostically most-relevant strains or species of a disease organism or
 CC to selectively amplify high-risk strains of an infectious organism. The
 CC present sequence is that of a HPV PNA probe which was used in the
 CC exemplification of the invention.
 XX SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 15; DB 12; Length 17;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AGATACCACACGCAG 15
 Db 2 AGATACCACACGCAG 16
 |||||
 |||||
 RESULT 5
 AA170570
 ID AA170570 standard; DNA; 22 BP.
 XX AC AA170570;
 XX DT 21-JAN-2002 (first entry)
 XX DE Human papillomavirus modified consensus primer MC01.
 XX KW HPV; probe; detection; typing; diagnosis; endocervical carcinoma;
 XX KW cervical cancer; neoplasia; PCR primer; ss.
 XX OS Human papillomavirus.
 XX PN WO200175174-A2.
 XX PD 11-OCT-2001.
 XX PF 03-APR-2001; 2001WO-US010795.
 XX PR 03-APR-2000; 2000US-0194304P.

PR 15-AUG-2000; 2000US-0225524P.
 XX (CVTY-) CYTVC CORP.
 XX PI Cohenford MA, Lentricchia B;
 XX DR WPI; 2001-648563/74.
 XX PT Detecting the presence of at least one selected strain of a disease
 XX PT organism or of a target nucleic acid of a human papilloma virus in a
 XX PT sample, comprises employing peptide-nucleic acid probes.
 XX PS Example 4; Page 25; 27pp; English.
 XX SQ The present sequence is that of human papillomavirus (HPV) modified
 CC consensus primer MC01. The primer was constructed for use with primer
 CC MY09 (see AAI70571) and is capable of amplifying multiple HPV strains,
 CC including strain 18. Use of probe VIII (see AAI70569) blocks
 CC amplification of HPV strain 18 DNA. The invention provides methods for
 CC the specific detection of high-risk type HPV nucleic acids. Patient
 CC samples, e.g. cervical scrapings, can be screened for the presence of a
 CC high-risk HPV variant, especially type 16, 18, 31, 33, 35, 39, 45, 51,
 CC 52, 56, 58, 59, 68 and 70. The presence of a particular target nucleic
 CC acid in sample cells is diagnostic of HPV infection, and may be
 CC indicative of risks of cancer, such as endocervical carcinoma, cervical
 CC cancer and neoplasia
 XX SQ Sequence 22 BP; 8 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 15; DB 5; Length 22;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AGATACCACACGCAG 15
 Db 7 AGATACCACACGCAG 21
 |||||
 |||||
 RESULT 6
 ADO08494
 ID ADO08494 standard; DNA; 22 BP.
 XX AC ADO08494;
 XX DT 12-AUG-2004 (first entry)
 XX DE Human papillomavirus (HPV) detection-related PCR primer MC01 SeqID26.
 XX KW detection; typing; Human Papilloma Virus; HPV; infection; PNA probe;
 XX KW high-risk; infectious organism; MC01; PCR; primer; ss.
 XX OS Human papillomavirus.
 XX PN WO2004042071-A2.
 XX PD 21-MAY-2004.
 XX PF 07-OCT-2003; 2003WO-US031841.
 XX PR 01-NOV-2002; 2002US-00286387.
 XX PA (CVTY-) CYTVC CORP.
 XX PI Cohenford MA, Lentricchia BB;
 XX DR WPI; 2004-400683/37.
 XX PT New peptide-nucleic acids, useful as a probe for detecting and typing
 XX PT Human Papilloma Virus infection, or in screening assay toward the
 XX PT diagnostically most-relevant strains or species of a disease organism.
 XX PS Example 4; SEQ ID NO 26; 26pp; English.

CC This invention relates to a novel method for detection and typing of a
 CC Human Papilloma Virus (HPV) infection using PNA primers or probes,
 CC including methods for detecting high-risk types of HPV infection with
 CC minimal numbers of PNA probes or using PNA primers to selectively amplify
 CC only high-risk types of HPV. Specifically claimed are novel primer/probe
 CC sequences which are useful as primers/probes for detecting and typing HPV
 CC infection. The methods are used in a screening assay toward the
 CC diagnostically most-relevant strains or species of a disease organism or
 CC to selectively amplify high-risk strains of an infectious organism. The
 CC present sequence is that of a PCR primer, MC01, which was used in the
 CC exemplification of the invention.
 XX
 SQ Sequence 22 BP; 8 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 12; Length 22;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15
 DB 7 AGATACCACACGCAG 21

RESULT 7
 AAQ56371
 ID AAQ56371 standard; DNA; 25 BP.

XX AC AAQ56371;

XX DT 25-MAR-2003 (revised)
 XX DT 29-JUL-1994 (first entry)

XX DE L1 consensus probe FS10.

XX KW Human papilloma virus; amplification; polymerase chain reaction; PCR;
 XX KW detection; assay; ss.

XX OS Synthetic.

XX PN US5283171-A.

XX PD 01-FEB-1994.

XX PF 15-FEB-1991; 91US-00651356.

XX PR 09-SEP-1988; 88US-00243486.

XX PR 10-MAR-1989; 89US-00322550.

XX PR 29-AUG-1989; 89WO-US003747.

XX PA (UYRP) UNIV ROCHESTER.

XX PA (HOFF) HOFFMANN LA ROCHE INC.

XX PI Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;

XX DR WPI; 1994-048082/06.

XX PT Detection of genital human papilloma virus - by PCR amplification using
 XX PT defined consensus primer pairs.

XX PS Disclosure; Page 6; 13pp; English.

XX CC The sequence is that of Ls1 consensus probe FS10 which was used as part
 XX CC of a simple and rapid assay method for detecting and typing HPV in
 XX CC biological samples. (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 25 BP; 7 A; 7 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15
 |||||

DB 8 AGATACCACACGCAG 22

RESULT 8
 AAQ56337
 ID AAQ56337 standard; DNA; 25 BP.

XX AC AAQ56337;

XX DT 25-MAR-2003 (revised)

XX DT 29-JUL-1994 (first entry)

XX DE Genital HPV L1 consensus positive strand primer FS10.

XX KW Human papilloma virus; amplification; polymerase chain reaction; PCR;
 XX KW detection; assay; ss.

XX OS Synthetic.

XX PN US5283171-A.

XX PD 01-FEB-1994.

XX PF 15-FEB-1991; 91US-00651356.

XX PR 09-SEP-1988; 88US-00243486.

XX PR 10-MAR-1989; 89US-00322550.

XX PR 29-AUG-1989; 89WO-US003747.

XX PA (UYRP) UNIV ROCHESTER.

XX PA (HOFF) HOFFMANN LA ROCHE INC.

XX PI Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;

XX DR WPI; 1994-048082/06.

XX PT Detection of genital human papilloma virus - by PCR amplification using
 XX PT defined consensus primer pairs.

XX PS Claim 5; Page 4; 13pp; English.

XX CC The sequence is that of the human papilloma virus (HPV) L1 consensus
 XX CC positive strand primer FS10 which was used in the amplification by PCR of
 XX CC HPV DNA. It may be used as part of a simple and rapid assay method for
 XX CC detecting and typing HPV in biological samples. (Updated on 25-MAR-2003
 XX CC to correct PF field.)

XX SQ Sequence 25 BP; 7 A; 7 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15
 |||||

DB 8 AGATACCACACGCAG 22

RESULT 9
 AAT44733
 ID AAT44733 standard; DNA; 25 BP.

XX AC AAT44733;

XX DT 25-MAR-2003 (revised)

XX DT 29-JAN-1997 (first entry)

XX DE L1 consensus positive strand primer FS10.

XX KW Probe; primer; PCR; polymerase chain reaction; amplification;
 XX KW human papillomavirus; consensus; ss.

XX OS Synthetic.

XX PN US5527898-A.
 XX PD 18-JUN-1996.
 XX PF 07-JUN-1995; 95US-00474542.
 XX PR 09-SEP-1988; 88US-00243486.
 XX PR 10-MAR-1989; 89US-00322550.
 XX PR 09-SEP-1989; 89WO-US003747.
 XX PR 14-NOV-1990; 90US-00613142.
 XX PR 20-APR-1993; 93US-00050743.
 XX PR 24-SEP-1993; 93US-00126452.
 XX PA (HOFF) HOFFMANN LA ROCHE INC.
 XX PI Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;
 XX PI WPI; 1996-299903/30.
 XX DR Nucleic acid hybridisation probes - specific for selected human papilloma
 XX PT virus types.
 XX PS Disclosure; Col 13-14; 96pp; English.
 XX CC The invention relates to new oligonucleotide probes and primers used for
 XX CC the detection of human papillomaviruses (HPV) which are not genital types
 XX CC 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
 XX CC to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
 XX CC primers can be used to detect these HPV types in conjunction with the
 XX CC consensus primers and typing probes AAT44733-T44906, which are based on
 XX CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
 XX CC sequences. This primer together with the negative strand primers AAT44736
 XX CC -7 amplifies a 1.1-1.4 kb region across the L1, URR (transcription
 XX CC regulatory region) and E6 regions from HPV types 6, 11, 16, 18 and 33.
 XX CC (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 25 BP; 7 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 15; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGATACCACACGCGAG 15
 Db 8 AGATACCACACGCGAG 22
 RESULT 10
 AAT77886
 ID AAT77886 standard; DNA; 25 BP.
 XX AC AAT77886;
 XX DT 25-MAR-2003 (revised)
 XX DT 06-OCT-1997 (first entry)
 XX DE Human papillomavirus probe FS10.
 XX KW Human; papillomavirus; HPV; probe; detection; ss.
 XX OS Synthetic.
 XX PN US5639871-A.
 XX PD 17-JUN-1997.
 XX PF 01-JUN-1995; 95US-00457648.
 XX PR 09-SEP-1988; 88US-00243486.
 XX PR 10-MAR-1989; 89US-00322550.
 XX PR 29-AUG-1989; 89WO-US003747.
 XX PR 14-NOV-1990; 90US-00613142.

PR 20-APR-1993; 93US-00050743.
 PR 24-SEP-1993; 93US-00126452.
 XX (HOFF) ROCHE MOLECULAR SYSTEMS INC.
 XX PI Imprim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;
 XX PI Gravitt PE;
 XX DR WPI; 1997-332084/30.
 XX PR New oligo:nucleotide probes for human papilloma-virus - used for
 XX PT detecting and typing HPV and for detecting previously unknown HPV types
 XX PT and subtypes.
 XX PS Disclosure; Col 69-70; 94pp; English.
 XX CC The present sequence is a human papillomavirus (HPV) specific probe.
 XX CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 XX CC correct PR field.)
 XX SQ Sequence 25 BP; 7 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 15; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGATACCACACGCGAG 15
 Db 8 AGATACCACACGCGAG 22
 RESULT 11
 AAV17472
 ID AAV17472 standard; DNA; 25 BP.
 XX AC AAV17472;
 XX DT 25-MAR-2003 (revised)
 XX DT 04-JUN-1998 (first entry)
 XX DE Primer FS10 for human papillomavirus typing.
 XX KW Human papillomavirus; HPV; HPV detection; HPV typing;
 XX KW L1 type-specific probe; PCR primer; ss.
 XX OS Synthetic.
 XX OS Human papillomavirus.
 XX PN US5705627-A.
 XX PD 06-JAN-1998.
 XX PF 26-MAY-1995; 95US-00452055.
 XX PR 09-SEP-1988; 88US-00243486.
 XX PR 10-MAR-1989; 89US-00322550.
 XX PR 14-NOV-1990; 90US-00613142.
 XX PR 20-APR-1993; 93US-00050743.
 XX PA (HOFF) ROCHE MOLECULAR SYSTEMS INC.
 XX PI Ting Y, Resnick RM, Greer CE, Bauer HM, Manos MM;
 XX PI WPI; 1998-192210/17.
 XX DR Human papilloma probes and primers - useful for, e.g. detecting and
 XX PT typing of human papilloma viruses.
 XX PS Disclosure; Col 5-6; 37pp; English.
 XX CC This sequence represents a human papillomavirus (HPV) L1 type-specific
 XX CC primer of the invention. This sequence may be used in conjunction with L1
 XX CC specific probes for detecting and typing HPV. Identification and typing

CC of HPV is important as different types of HPV pose different risks for
 CC infected individuals. HPV16 and HPV18 have been more consistently
 CC identified in higher grades of cervical dysplasia and carcinoma than
 CC other HPV types. (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 25 BP; 7 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 15; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGATACCACACGCAG 15
 |||||
 Db 8 AGATACCACACGCAG 22

RESULT 12
 AAQ87034
 ID AAQ87034 standard; DNA; 26 BP.
 XX
 AC AAQ87034;
 XX
 DT 12-JAN-1996 (first entry)
 XX
 DE Oligonucleotide probe to identify HPV 11 late genes.
 XX probe; hybridisation; human papilloma virus; HPV; detection; riboprobe;
 KW diagnosis; ss.
 OS Synthetic.
 XX
 PN WO9511316-A1.
 XX
 PD 27-APR-1995.
 XX
 PF 19-OCT-1994; 94WO-US012044.
 XX
 PR 22-OCT-1993; 93US-00141711.
 XX (AMGE-) AMGEN INC.
 PA
 PI Martin FH, Jacobsen FW, Green CL;
 XX
 DR WPI; 1995-193795/25.
 XX
 PT Detection of target nucleic acid sequence in biological samples - using a
 PT labelled riboprobe which hybridises to target nucleic acid for use in
 PT medical diagnostics, forensics, and research.
 XX
 PS Example 1; Page 37; 75pp; English.
 XX
 CC The probe was 32P-end labeled and added to a HPV 11 sample to identify
 CC late genes. Hybridisation was conducted and plaques contg. DNA mols.
 CC complementary to the probe were identified. The plaques were probed also
 CC with a probe for early genes (AAQ87035). Positive plaques hybridised to
 CC both early and late probes. DNA was prepd. for the prodn. of riboprobes
 CC to be used in the methods of the invention. Riboprobes improve the
 CC detection limits of nucleic acid hybridisation. The detection methods
 CC using riboprobes can be used in medical diagnostics, forensics and
 CC molecular biology research
 XX
 SQ Sequence 26 BP; 8 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 15; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGATACCACACGCAG 15
 |||||
 Db 9 AGATACCACACGCAG 23

RESULT 13

AAT10813
 ID AAT10813 standard; DNA; 25 BP.
 XX
 AC AAT10813;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-APR-1996 (first entry)
 XX
 DE Human papilloma virus L1 region consensus probe MY46.
 XX
 KW Human papilloma virus; probe; detection; diagnosis; genital; oral;
 KW carcinomas; research; L1 region; consensus; MY46; ss.
 XX
 OS Synthetic.
 XX
 PN US5447839-A.
 XX
 PD 05-SEP-1995.
 XX
 PF 20-APR-1993; 93US-00050743.
 XX
 PR 09-SEP-1988; 88US-00243486.
 PR 10-MAR-1989; 89US-00322550.
 PR 09-SEP-1989; 89WO-US003747.
 PR 14-NOV-1990; 90US-00613142.
 XX
 PA (HOFF) HOFFMANN LA ROCHE INC.
 XX
 PI Ting Y, Resnick RM, Greer CE, Manos MM, Bauer HM;
 XX WPI; 1995-319884/41.
 XX
 PT Detection of human papilloma virus DNA by amplification - using specific
 PT consensus primer pairs and pref. detection with generic or type specific
 PT probes for use in research and diagnosis.
 XX
 PS Claim 2; Col 33-34; 36pp; English.
 XX
 CC A human papilloma virus (HPV) L1 region consensus probe comprising an
 CC equimolar mix of the probes AAT10812-15, was used to detect HPV for
 CC research or diagnostic purposes, e.g. to identify HPV that are implicated
 CC in genital or oral carcinomas. (Updated on 25-MAR-2003 to correct PF
 CC field.)
 XX
 SQ Sequence 25 BP; 6 A; 7 C; 6 G; 5 T; 0 U; 1 Other;
 Query Match 97.3%; Score 14.6; DB 2; Length 25;
 Best Local Similarity 93.3%; Pred. No. 1.6e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGATACCACACGCAG 15
 |||||
 Db 8 AGATACCACACGCAG 22

RESULT 14
 AAT44761
 ID AAT44761 standard; DNA; 25 BP.
 XX
 AC AAT44761;
 XX
 DT 25-MAR-2003 (revised)
 DT 29-JAN-1997 (first entry)
 XX
 DE L1 consensus probe MY46.
 XX Probe; primer; PCR; polymerase chain reaction; amplification;
 KW human papillomavirus; consensus; ss.
 XX
 OS Synthetic.
 XX
 PN US527898-A.
 XX

PD 18-JUN-1996.
 XX 07-JUN-1995; 95US-00474542.
 XX 09-SEP-1988; 88US-00243486.
 PR 10-MAR-1989; 89US-00322550.
 PR 09-SEP-1989; 89WO-US003747.
 PR 14-NOV-1990; 90US-00613142.
 PR 20-APR-1993; 93US-00050743.
 PR 24-SEP-1993; 93US-00126452.
 XX (HOFF) HOFFMANN LA ROCHE INC.
 XX Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;
 PI WPI; 1996-299903/30.
 DR Nucleic acid hybridisation probes - specific for selected human papilloma
 PT virus types.
 XX Disclosure; Col 29-30; 96pp; English.
 XX The invention relates to new oligonucleotide probes and primers used for
 CC the detection of human papillomaviruses (HPV) which are not genital types
 CC 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
 CC to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
 CC primers can be used to detect these HPV types in conjunction with the
 CC consensus primers and typing probes AAT44733-T44906, which are based on
 CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
 CC sequences. Detection of the amplification prods. is done with probes
 CC derived from consensus sequences found in all characterised HPV
 CC sequences. The probes AAT44755-61 are examples of L1 consensus probes for
 CC identifying the amplified products. (Updated on 25-MAR-2003 to correct PF
 CC field.)
 XX SQ Sequence 25 BP; 6 A; 7 C; 6 G; 5 T; 0 U; 1 Other;
 Query Match 97.3%; Score 14.6; DB 2; Length 25;
 Best Local Similarity 93.3%; Pred. No. 1.6e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AGATACCACACGCGAG 15
 Db 8 AGATACCACACGCGAG 22
 RESULT 15
 AAT77893
 ID AAT77893 standard; DNA; 25 BP.
 XX AC AAT77893;
 XX 25-MAR-2003 (revised)
 DT 06-OCT-1997 (first entry)
 XX Human papillomavirus probe MY46.
 DE Human, papillomavirus; HPV; probe; detection; ss.
 XX Synthetic.
 XX US5639871-A.
 PN 17-JUN-1997.
 PD 01-JUN-1995; 95US-00457648.
 XX 09-SEP-1988; 88US-00243486.
 PR 10-MAR-1989; 89US-00322550.
 PR 29-AUG-1989; 89WO-US003747.
 PR 14-NOV-1990; 90US-00613142.
 PR 20-APR-1993; 93US-00050743.
 PR 24-SEP-1993; 93US-00126452.

XX (HOFF) ROCHE MOLECULAR SYSTEMS INC.
 XX Imprim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;
 PI Gravitt PE;
 XX WPI; 1997-332084/30.
 XX New oligo:nucleotide probes for human papilloma-virus - used for
 PT detecting and typing HPV and for detecting previously unknown HPV types
 PT and subtypes.
 XX Disclosure; Col 71-72; 94pp; English.
 XX The present sequence is a human papillomavirus (HPV) specific probe.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 CC correct PR field.)
 XX SQ Sequence 25 BP; 6 A; 7 C; 6 G; 5 T; 0 U; 1 Other;
 Query Match 97.3%; Score 14.6; DB 2; Length 25;
 Best Local Similarity 93.3%; Pred. No. 1.6e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AGATACCACACGCGAG 15
 Db 8 AGATACCACACGCGAG 22
 Search completed: June 23, 2005, 18:24:36
 Job time : 421 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 18:05:30 ; Search time 123 Seconds
(without alignments)
199.546 Million cell updates/sec

Title: US-09-825-482-6

Perfect score: 15

Sequence: 1 agataccacacgcag 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 970836

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*
 - 2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*
 - 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
 - 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
 - 5: /cgn2_6/ptodata/1/ina/PTCTUS COMB.seq:*
 - 6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 15 | 100.0 | 25 | 1 | US-08-474-542A-21 |
| 2 | 15 | 100.0 | 25 | 1 | US-08-457-648-21 |
| 3 | 14.6 | 97.3 | 25 | 1 | US-08-050-743-9 |
| 4 | 14.6 | 97.3 | 25 | 1 | US-08-474-542A-28 |
| 5 | 14.6 | 97.3 | 25 | 1 | US-08-457-648-28 |
| 6 | 14.6 | 97.3 | 25 | 1 | US-08-452-055-9 |
| 7 | 13.4 | 89.3 | 25 | 1 | US-08-474-542A-26 |
| 8 | 13.4 | 89.3 | 25 | 1 | US-08-474-542A-271 |
| 9 | 13.4 | 89.3 | 25 | 1 | US-08-457-648-26 |
| 10 | 13.4 | 89.3 | 25 | 1 | US-08-457-648-271 |
| 11 | 13 | 86.7 | 21 | 1 | US-07-722-788A-75 |
| 12 | 13 | 86.7 | 22 | 1 | US-07-722-788A-76 |
| 13 | 12.4 | 82.7 | 25 | 1 | US-08-474-542A-106 |
| 14 | 12.4 | 82.7 | 25 | 1 | US-08-457-648-106 |
| 15 | 12.4 | 82.7 | 25 | 3 | US-08-155-938-35 |
| 16 | 12.4 | 82.7 | 27 | 3 | US-08-155-938-34 |
| 17 | 11.8 | 78.7 | 25 | 1 | US-08-474-542A-22 |
| 18 | 11.8 | 78.7 | 25 | 1 | US-08-457-648-22 |
| 19 | 11.8 | 78.7 | 25 | 4 | US-09-396-196G-57331 |
| 20 | 11.4 | 76.0 | 24 | 4 | US-08-899-112B-14 |
| 21 | 11.4 | 76.0 | 24 | 4 | US-09-011-553-15 |
| 22 | 11.4 | 76.0 | 25 | 4 | US-09-396-196G-14509 |
| 23 | 11.4 | 76.0 | 25 | 4 | US-09-396-196G-57330 |
| 24 | 11 | 73.3 | 23 | 3 | US-08-338-579A-70 |
| 25 | 11 | 73.3 | 23 | 5 | PCT-US94-09851-70 |
| 26 | 10.8 | 72.0 | 20 | 4 | US-09-198-452A-6764 |
| 27 | 10.8 | 72.0 | 20 | 4 | US-09-033-936-71 |

| | | | | | | | |
|---|----|------|------|----|---|-----------------------|--------------------|
| c | 28 | 10.8 | 72.0 | 24 | 4 | US-09-705-872-8 | Sequence 8, Appli |
| c | 29 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-4231 | Sequence 4231, Ap |
| | 30 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-10749 | Sequence 10749, A |
| | 31 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-10750 | Sequence 10750, A |
| | 32 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-44088 | Sequence 44088, A |
| | 33 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-44089 | Sequence 44089, A |
| | 34 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-54438 | Sequence 54438, A |
| | 35 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-54439 | Sequence 54439, A |
| | 36 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-65875 | Sequence 65875, A |
| | 37 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-88276 | Sequence 88276, A |
| | 38 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-90071 | Sequence 90071, A |
| | 39 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-100045 | Sequence 100045, A |
| | 40 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-100047 | Sequence 100047, A |
| | 41 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-100048 | Sequence 100048, A |
| | 42 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-111377 | Sequence 111377, A |
| | 43 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-111378 | Sequence 111378, A |
| | 44 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-111394 | Sequence 111394, A |
| | 45 | 10.8 | 72.0 | 25 | 4 | US-09-396-196G-111395 | Sequence 111395, A |

ALIGNMENTS

RESULT 1
US-08-474-542A-21
Sequence 21, Application US/08474542A
Patent No. 5527898
GENERAL INFORMATION:
APPLICANT: Bauer, Heidi M.
APPLICANT: Gravitt, Patti E.
APPLICANT: Greer, Catherine E.
APPLICANT: Imprim, Chaka C.
APPLICANT: Manos, M. Michele
APPLICANT: Resnick, Robert M.
TITLE OF INVENTION: Detection of Human Papillomavirus by the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 298
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,542A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-474-542A-21

Query Match 100.0%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AGATACCACGCAG 15
Db 8 AGATACCACGCAG 22

RESULT 2
US-08-457-648-21
; Sequence 21, Application US/08457648
; Patent No. 5639871
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraime, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-457-648-21

Query Match 100.0%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACGCAG 15
Db 8 AGATACCACGCAG 22

RESULT 3
US-08-050-743-9
; Sequence 9, Application US/08050743
; Patent No. 5447839
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Manos, Michele
; APPLICANT: Resnick, Robert M.
; APPLICANT: Ting, Yi
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; NUMBER OF SEQUENCES: 85
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,743
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias, Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-050-743-9

Query Match 97.3%; Score 14.6; DB 1; Length 25;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACGCAG 15
Db 8 AGATACCACGCAG 22

RESULT 4
US-08-474-542A-28
; Sequence 28, Application US/08474542A
; Patent No. 5527898
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraime, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,542A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
```

REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-474-542A-28

Query Match 97.3%; Score 14.6; DB 1; Length 25;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACGCGAG 15
Db 8 AGATACCACGCGAG 22

RESULT 5
US-08-457-648-28
; Sequence 28, Application US/08457648
; Patent No. 5639871
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravit, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Imprim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/457,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-457-648-28

Query Match 97.3%; Score 14.6; DB 1; Length 25;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACGCGAG 15
Db 8 AGATACCACGCGAG 22

RESULT 6
US-08-452-055-9
; Sequence 9, Application US/08452055
; Patent No. 5705627
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Manos, Michele
; APPLICANT: Resnick, Robert M.
; APPLICANT: Ting, Yi
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/452,055
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias, Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 9188
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-452-055-9

Query Match 97.3%; Score 14.6; DB 1; Length 25;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACGCGAG 15
Db 8 AGATACCACGCGAG 22

RESULT 7
US-08-474-542A-26
; Sequence 26, Application US/08474542A
; Patent No. 5527898
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravit, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Imprim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,542A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2977
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-542A-26

Query Match      89.3%; Score 13.4; DB 1; Length 25;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AGATACCACGCGAG 15
Db      8 AGATACCACGCTAG 22

RESULT 8
US-08-474-542A-271
; Sequence 271, Application US/08474542A
; Patent No. 5527898
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraïm, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,542A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-457-648-26
```

```
;
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 271:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-542A-271

Query Match      89.3%; Score 13.4; DB 1; Length 25;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AGATACCACGCGAG 15
Db      8 AGATACCACGCGAG 22

RESULT 9
US-08-457-648-26
; Sequence 26, Application US/08457648
; Patent No. 5639871
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraïm, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-457-648-26

Query Match      89.3%; Score 13.4; DB 1; Length 25;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```


Qy 1 AGATACCACGCGAG 15
 Db 8 AGATACCACGCGAG 22

RESULT 10

US-08-457-648-271
 ; Sequence 271, Application US/08457648
 ; Patent No. 5639871
 ; GENERAL INFORMATION:
 ; APPLICANT: Bauer, Heidi M.
 ; APPLICANT: Gravit, Fatti E.
 ; APPLICANT: Greer, Catherine E.
 ; APPLICANT: Impra, Chaka C.
 ; APPLICANT: Manos, M. Michele
 ; APPLICANT: Resnick, Robert M.
 ; TITLE OF INVENTION: Detection of Human Papillomavirus by the
 ; TITLE OF INVENTION: Polymerase Chain Reaction
 ; NUMBER OF SEQUENCES: 298
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hoffmann-La Roche Inc.
 ; STREET: 340 Kingsland Street
 ; CITY: Nutley
 ; STATE: New Jersey
 ; COUNTRY: U.S.A.
 ; ZIP: 07110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/457,648
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Petry, Douglas A.
 ; REGISTRATION NUMBER: 35,321
 ; REFERENCE/DOCKET NUMBER: 9205
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (510) 814-2974
 ; TELEFAX: (510) 814-2977
 ; INFORMATION FOR SEQ ID NO: 271:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-457-648-271

Query Match 89.3%; Score 13.4; DB 1; Length 25;
 Best Local Similarity 93.3%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGATACCACGCGAG 15
 Db 8 AGATACCACGCGAG 22

RESULT 11

US-07-722-798A-75
 ; Sequence 75, Application US/07722798A
 ; Patent No. 5427930
 ; GENERAL INFORMATION:
 ; APPLICANT: Larry G. Birkenmeyer
 ; APPLICANT: John J. Carrino
 ; APPLICANT: Bruce J. Dille
 ; APPLICANT: Hsiang-Yun Hu
 ; APPLICANT: Jon David Kratochvil
 ; APPLICANT: Thomas G. Laffler
 ; APPLICANT: Ronald L. Marshall
 ; APPLICANT: Laurie A. Rinehardt

APPLICANT: Natalie A. Solomon
 TITLE OF INVENTION: AMPLIFICATION OF TARGET NUCLEIC
 TITLE OF INVENTION: ACIDS USING GAP FILLING LIGASE CHAIN REACTION
 NUMBER OF SEQUENCES: 124
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: One Abbott Park Road
 CITY: Abbott Park
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/722,798A
 FILING DATE: 19910628
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Thomas D. Brainard
 REGISTRATION NUMBER: 32,459
 REFERENCE/DOCKET NUMBER: 4773.US.P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-4884
 TELEFAX: 708-937-9556
 INFORMATION FOR SEQ ID NO: 75:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Other nucleic acid (synthetic DNA)
 US-07-722-798A-75

Query Match 86.7%; Score 13; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GATACCACGCA 14
 Db 9 GATACCACGCA 21

RESULT 12

US-07-722-798A-76/c
 ; Sequence 76, Application US/07722798A
 ; Patent No. 5427930
 ; GENERAL INFORMATION:
 ; APPLICANT: Larry G. Birkenmeyer
 ; APPLICANT: John J. Carrino
 ; APPLICANT: Bruce J. Dille
 ; APPLICANT: Hsiang-Yun Hu
 ; APPLICANT: Jon David Kratochvil
 ; APPLICANT: Thomas G. Laffler
 ; APPLICANT: Ronald L. Marshall
 ; APPLICANT: Laurie A. Rinehardt
 ; APPLICANT: Natalie A. Solomon
 TITLE OF INVENTION: AMPLIFICATION OF TARGET NUCLEIC
 TITLE OF INVENTION: ACIDS USING GAP FILLING LIGASE CHAIN REACTION
 NUMBER OF SEQUENCES: 124
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: One Abbott Park Road
 CITY: Abbott Park
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

```
; SOFTWARE: Wordperfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/722,798A
; FILING DATE: 19910628
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 4773.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-4884
; TELEFAX: 708-937-9556
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-07-722-798A-76

Query Match      86.7%; Score 13; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GATACCACGCGCA 14
      |||||
Db      13 GATACCACGCGCA 1

RESULT 13
US-08-474-542A-106
; Sequence 106, Application US/08474542A
; Patent No. 5527898
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,542A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-474-542A-106

Query Match      82.7%; Score 12.4; DB 1; Length 25;
Best Local Similarity 92.9%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GATACCACGCGAG 15
      |||||
Db      9 GATACCACGCGAG 22

RESULT 14
US-08-457-648-106
; Sequence 106, Application US/08457648
; Patent No. 5639871
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-457-648-106

Query Match      82.7%; Score 12.4; DB 1; Length 25;
Best Local Similarity 92.9%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GATACCACGCGAG 15
      |||||
Db      9 GATACCACGCGAG 22

RESULT 15
US-08-155-938-35
; Sequence 35, Application US/08155938
; Patent No. 6004826
; GENERAL INFORMATION:
; APPLICANT: Segev, David
```

TITLE OF INVENTION: PROCESS FOR AMPLIFYING AND DETECTING
 TITLE OF INVENTION: NUCLEIC ACID SEQUENCES
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: InClone Systems Incorporated
 STREET: 180 Varlick Street
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10014
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/155,938
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/841,649
 FILING DATE:
 APPLICATION NUMBER: US 07/221,750
 FILING DATE: 20-JUL-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/784,749
 FILING DATE: 28-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Feit, Irving N.
 REGISTRATION NUMBER: 28,601
 REFERENCE/DOCKET NUMBER: SEG-1-CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-645-1405
 TELEFAX: 212-645-2054
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-155-938-35

Query Match 82.7%; Score 12.4; DB 3; Length 25;
 Best Local Similarity 92.9%; Pred. No. 7.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GATACACACGAG 15
 |||||
 Db 9 GATACACACGAG 22

Search completed: June 23, 2005, 19:44:46
 Job time : 124 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 18:17:36 ; Search time 520 Seconds
(without alignments)
180.303 Million cell updates/sec

Title: US-09-825-482-6

Perfect score: 15

Sequence: 1 agataccacacgcag 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters: 5576672

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA: *
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 - 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
 - 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
 - 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
 - 12: /cgn2_6/ptodata/1/pubpna/US09D_PUBCOMB.seq:*
 - 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
 - 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
 - 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
 - 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
 - 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
 - 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
 - 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
 - 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
 - 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
 - 22: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq:*
 - 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
 - 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
 - 25: /cgn2_6/ptodata/1/pubpna/US16_NEW_PUB.seq:*
 - 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 15 | 100.0 | 15 | 9 | US-09-825-482-6 |
| 2 | 15 | 100.0 | 15 | 15 | US-10-323-188-6 |
| 3 | 15 | 100.0 | 15 | 15 | US-10-286-387-23 |
| 4 | 15 | 100.0 | 17 | 9 | US-09-825-482-7 |
| 5 | 15 | 100.0 | 17 | 15 | US-10-323-188-7 |
| 6 | 15 | 100.0 | 17 | 15 | US-10-286-387-24 |
| 7 | 15 | 100.0 | 22 | 9 | US-09-825-482-9 |

| | | | | | | | |
|--------------------|----|----|-------|----|----|----------------------|--------------------|
| Sequence 9, Appli | 22 | 15 | 100.0 | 22 | 15 | US-10-323-188-9 | Sequence 9, Appli |
| Sequence 26, Appli | 22 | 15 | 100.0 | 22 | 15 | US-10-286-387-26 | Sequence 26, Appli |
| Sequence 842484, | 25 | 21 | 89.3 | 25 | 21 | US-10-719-900-842484 | Sequence 842484, |
| Sequence 882687, | 25 | 21 | 89.3 | 25 | 21 | US-10-719-900-882687 | Sequence 882687, |
| Sequence 964593, | 25 | 21 | 89.3 | 25 | 21 | US-10-719-900-964593 | Sequence 964593, |
| Sequence 3, Appli | 14 | 9 | 82.7 | 14 | 9 | US-09-825-482-3 | Sequence 3, Appli |
| Sequence 3, Appli | 14 | 15 | 82.7 | 14 | 15 | US-10-323-188-3 | Sequence 3, Appli |
| Sequence 3, Appli | 14 | 15 | 82.7 | 14 | 15 | US-10-286-387-3 | Sequence 3, Appli |
| Sequence 70330, A | 25 | 15 | 82.7 | 25 | 15 | US-10-098-263B-70330 | Sequence 70330, A |
| Sequence 1035, Ap | 25 | 15 | 82.7 | 25 | 15 | US-10-719-900-1035 | Sequence 1035, Ap |
| Sequence 45007, A | 25 | 21 | 82.7 | 25 | 21 | US-10-719-900-45007 | Sequence 45007, A |
| Sequence 45008, A | 25 | 21 | 82.7 | 25 | 21 | US-10-719-900-45008 | Sequence 45008, A |
| Sequence 501938, | 25 | 21 | 82.7 | 25 | 21 | US-10-719-900-501938 | Sequence 501938, |
| Sequence 707395, | 25 | 21 | 82.7 | 25 | 21 | US-10-719-900-707395 | Sequence 707395, |
| Sequence 768545, | 25 | 21 | 82.7 | 25 | 21 | US-10-719-900-768545 | Sequence 768545, |
| Sequence 68055, A | 25 | 21 | 82.7 | 25 | 21 | US-10-956-157-68055 | Sequence 68055, A |
| Sequence 126114, | 25 | 21 | 82.7 | 25 | 21 | US-10-956-157-126114 | Sequence 126114, |
| Sequence 463970, | 25 | 21 | 80.0 | 25 | 21 | US-10-719-900-463970 | Sequence 463970, |
| Sequence 463971, | 25 | 21 | 80.0 | 25 | 21 | US-10-719-900-463971 | Sequence 463971, |
| Sequence 857602, | 25 | 21 | 80.0 | 25 | 21 | US-10-719-900-857602 | Sequence 857602, |
| Sequence 8, Appli | 15 | 9 | 78.7 | 15 | 9 | US-09-825-482-8 | Sequence 8, Appli |
| Sequence 25, Appli | 15 | 15 | 78.7 | 15 | 15 | US-10-323-188-8 | Sequence 25, Appli |
| Sequence 34, Appli | 20 | 19 | 78.7 | 20 | 19 | US-10-286-387-25 | Sequence 34, Appli |
| Sequence 34, Appli | 20 | 19 | 78.7 | 20 | 19 | US-10-361-002-34 | Sequence 34, Appli |
| Sequence 12909, A | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-12909 | Sequence 12909, A |
| Sequence 46150, A | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-46150 | Sequence 46150, A |
| Sequence 97970, A | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-97970 | Sequence 97970, A |
| Sequence 99463, A | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-99463 | Sequence 99463, A |
| Sequence 158555, | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-158555 | Sequence 158555, |
| Sequence 158567, | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-158567 | Sequence 158567, |
| Sequence 167555, | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-167555 | Sequence 167555, |
| Sequence 207951, | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-207951 | Sequence 207951, |
| Sequence 224387, | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-224387 | Sequence 224387, |
| Sequence 229611, | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-229611 | Sequence 229611, |
| Sequence 229612, | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-229612 | Sequence 229612, |
| Sequence 276617, | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-276617 | Sequence 276617, |
| Sequence 388065, | 25 | 21 | 78.7 | 25 | 21 | US-10-719-900-388065 | Sequence 388065, |

ALIGNMENTS

RESULT 1

US-09-825-482-6 Application US/09825482
; Sequence 6, Appli US/09825482
; Patent No. US20020155427A1
; GENERAL INFORMATION:
; APPLICANT: Lentricchia, Brian
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
; FILE REFERENCE: CVM-035
; CURRENT APPLICATION NUMBER: US/09/825,482
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,304
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/225,524
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA Probe VI
US-09-825-482-6

Query Match 100.0%; Score 15; DB 9; Length 15;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 1 AGATACCACACGCAG 15

FILE REFERENCE: cym-035CP
 CURRENT APPLICATION NUMBER: US/10/286,387
 CURRENT FILING DATE: 2003-02-28
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 24
 LENGTH: 17
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: PNA probe
 US-10-286-387-24

Query Match 100.0%; Score 15; DB 15; Length 17;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACACGCAG 15
 Db 2 AGATACCACACGCAG 16

RESULT 7
 US-09-825-482-9
 Sequence 9, Application US/09825482
 Patent No. US20020155427A1
 GENERAL INFORMATION:
 APPLICANT: Cohenford, Menashi
 APPLICANT: Lentricchia, Brian
 TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
 FILE REFERENCE: cym-035
 CURRENT APPLICATION NUMBER: US/09/825,482
 CURRENT FILING DATE: 2001-04-03
 PRIOR APPLICATION NUMBER: US 60/194,304
 PRIOR FILING DATE: 2000-04-03
 PRIOR APPLICATION NUMBER: US 60/225,524
 PRIOR FILING DATE: 2000-08-15
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 9
 LENGTH: 22
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: MC01 HPV consensus primer sequence
 US-09-825-482-9

Query Match 100.0%; Score 15; DB 9; Length 22;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACACGCAG 15
 Db 7 AGATACCACACGCAG 21

RESULT 8
 US-10-323-188-9
 Sequence 9, Application US/1023188
 Publication No. US20030108866A1
 GENERAL INFORMATION:
 APPLICANT: Cohenford, Menashi
 APPLICANT: Lentricchia, Brian
 TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
 FILE REFERENCE: cym-035DV
 CURRENT APPLICATION NUMBER: US/10/323,188
 CURRENT FILING DATE: 2002-12-18
 PRIOR APPLICATION NUMBER: 09/825,482
 PRIOR FILING DATE: 2001-04-03
 PRIOR APPLICATION NUMBER: US 60/194,304
 PRIOR FILING DATE: 2000-04-03
 PRIOR APPLICATION NUMBER: US 60/225,524
 PRIOR FILING DATE: 2000-08-15

NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 9
 LENGTH: 22
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: MC01 HPV consensus primer sequence
 US-10-323-188-9

Query Match 100.0%; Score 15; DB 15; Length 22;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACACGCAG 15
 Db 7 AGATACCACACGCAG 21

RESULT 9
 US-10-286-387-26
 Sequence 26, Application US/10286387
 Publication No. US20030143529A1
 GENERAL INFORMATION:
 APPLICANT: Cytoc Corporation
 TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
 FILE REFERENCE: cym-035CP
 CURRENT APPLICATION NUMBER: US/10/286,387
 CURRENT FILING DATE: 2003-02-28
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 26
 LENGTH: 22
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Modified consensus primer for amplifying multiple HPV strains
 US-10-286-387-26

Query Match 100.0%; Score 15; DB 15; Length 22;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACACGCAG 15
 Db 7 AGATACCACACGCAG 21

RESULT 10
 US-10-719-900-842484
 Sequence 842484, Application US/10719900
 Publication No. US20050026164A1
 GENERAL INFORMATION:
 APPLICANT: Xue Mei
 TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 FILE REFERENCE: 3528.1
 CURRENT APPLICATION NUMBER: US/10/719,900
 CURRENT FILING DATE: 2003-11-20
 PRIOR APPLICATION NUMBER: 60/427,808
 PRIOR FILING DATE: 2002-11-20
 NUMBER OF SEQ ID NOS: 982914
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO 842484
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Mus musculus
 US-10-719-900-842484

Query Match 89.3%; Score 13.4; DB 21; Length 25;
 Best Local Similarity 93.3%; Pred. No. 7.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGATACCACACGCAG 15

```
Db      8 AGATACCACGCGAG 22
|||||
RESULT 11
US-10-719-900-882687
; Sequence 882687, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 882687
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-882687

Query Match      89.3%; Score 13.4; DB 21; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AGATACCACGCGAG 15
|||||
Db      8 AGATACCACACCCGAG 22

RESULT 12
US-10-719-900-964593
; Sequence 964593, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 964593
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-964593

Query Match      89.3%; Score 13.4; DB 21; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AGATACCACGCGAG 15
|||||
Db      4 AGATAACACGCGAG 18

RESULT 13
US-09-825-482-3
; Sequence 3, Application US/09825482
; Patent No. US20020155427A1
; GENERAL INFORMATION:
; APPLICANT: Cohenford, Menashi
; APPLICANT: Lentrichia, Brian
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
; FILE REFERENCE: CYM-035
; CURRENT APPLICATION NUMBER: US/09/825,482
; CURRENT FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: US 60/194,304
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/225,524
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA Probe III
US-10-323-188-3

Query Match      82.7%; Score 12.4; DB 15; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GATACCACGCGAG 15
|||||
Db      1 GATACCACCTCGCAG 14

RESULT 14
US-10-323-188-3
; Sequence 3, Application US/10323188
; Publication No. US20030108866A1
; GENERAL INFORMATION:
; APPLICANT: Cohenford, Menashi
; APPLICANT: Lentrichia, Brian
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
; FILE REFERENCE: CYM-035DV
; CURRENT APPLICATION NUMBER: US/10/323,188
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 09/825,482
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,304
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/225,524
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA Probe III
US-10-323-188-3

Query Match      82.7%; Score 12.4; DB 15; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GATACCACGCGAG 15
|||||
Db      1 GATACCACCTCGCAG 14

RESULT 15
US-10-286-387-3
; Sequence 3, Application US/10286387
; Publication No. US20030143529A1
; GENERAL INFORMATION:
; APPLICANT: Cytoc Corporation
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
; FILE REFERENCE: CYM-035CP
; CURRENT APPLICATION NUMBER: US/10/286,387
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 14
```



```

; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PNA probe
US-10-286-387-3
Query Match      82.7%  Score 12.4; DB 15; Length 14;
Best Local Similarity 92.9%  Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy .      2 GATACCAACGCGAG 15
      |||||
Db      1 GATACCACTCGCGAG 14

```

Search completed: June 23, 2005, 19:53:38
Job time : 521 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 17:50:22 ; Search time 2981 Seconds
(without alignments)
191.534 Million cell updates/sec

Title: US-09-825-482-6

Perfect score: 15

Sequence: 1 agataccacacgcag 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 46888

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hcc.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gsl.*
- 9: gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|--------|----|-----------|---------------------|
| C 1 | 10.8 | 72.0 | 24 | 7 | L32033 | L32033 HUMXP11B6B |
| 2 | 10.4 | 69.3 | 24 | 8 | AZ794953 | AZ794953 2M0048N21 |
| 3 | 10.4 | 69.3 | 26 | 8 | BH792752 | BH792752 SALK_0649 |
| 4 | 10.4 | 69.3 | 30 | 9 | BX896975 | BX896975 Arabidops |
| C 5 | 10 | 66.7 | 20 | 8 | AZ782314 | AZ782314 2M0022D03 |
| 6 | 10 | 66.7 | 22 | 9 | TA205F05Q | TA205F05Q T. brucei |
| 7 | 10 | 66.7 | 23 | 9 | TA313C04P | TA313C04P T. brucei |
| C 8 | 10 | 66.7 | 25 | 1 | A1664044 | A1664044 ue73e05.r |
| C 9 | 9.8 | 65.3 | 20 | 8 | AZ770749 | AZ770749 1M0572B01 |
| 10 | 9.4 | 62.7 | 20 | 8 | AZ307506 | AZ307506 1M0009I16 |
| 11 | 9.4 | 62.7 | 22 | 8 | AZ346725 | AZ346725 1M0082P06 |
| 12 | 9.4 | 62.7 | 28 | 1 | A1613292 | A1613292 ty35g02.x |
| 13 | 9.2 | 61.3 | 20 | 8 | AZ8332127 | AZ8332127 2M0112M17 |
| C 14 | 9.2 | 61.3 | 21 | 8 | AZ510254 | AZ510254 1M0354F10 |
| C 15 | 9.2 | 61.3 | 22 | 8 | AZ309912 | AZ309912 1M0017P15 |
| C 16 | 9.2 | 61.3 | 23 | 8 | AZ501123 | AZ501123 1M0339A22 |
| 17 | 9.2 | 61.3 | 25 | 1 | A1024239 | A1024239 ov71g02.s |
| 18 | 9.2 | 61.3 | 27 | 1 | AU010622 | AU010622 AU010622 |
| C 19 | 9.2 | 61.3 | 27 | 8 | AZ779966 | AZ779966 2M0016C21 |
| C 20 | 9.2 | 61.3 | 27 | 9 | AG190440 | AG190440 Pan trogl |
| 21 | 9.2 | 61.3 | 28 | 1 | AA912344 | AA912344 ol97h02.s |
| 22 | 9.2 | 61.3 | 28 | 7 | CO784963 | CO784963 BL282A.F1 |
| C 23 | 9.2 | 61.3 | 29 | 8 | AZ956741 | AZ956741 2M0223C24 |
| 24 | 9.2 | 61.3 | 30 | 8 | AZ348488 | AZ348488 1M0085L06 |

| | | | | | | |
|------|-----|------|----|---|-----------|---------------------|
| C 25 | 9.2 | 61.3 | 30 | 8 | AZ588091 | AZ588091 1M0396K03 |
| C 26 | 9.2 | 61.3 | 30 | 9 | CL523751 | CL523751 DAL5G03.F |
| 27 | 9.0 | 60.0 | 20 | 8 | AZ628029 | AZ628029 1M0476F17 |
| 28 | 9 | 60.0 | 24 | 8 | AZ812858 | AZ812858 2M0079B21 |
| C 29 | 9 | 60.0 | 25 | 8 | AZ872633 | AZ872633 2M0186K01 |
| 30 | 9 | 60.0 | 26 | 8 | AZ435264 | AZ435264 1M0222G12 |
| 31 | 9 | 60.0 | 28 | 1 | AI037937 | AI037937 ox53all.x |
| C 32 | 8.8 | 58.7 | 19 | 8 | AZ651803 | AZ651803 1M0522N11 |
| 33 | 8.8 | 58.7 | 20 | 8 | AZ776456 | AZ776456 2M0010O03 |
| C 34 | 8.8 | 58.7 | 21 | 8 | AZ769838 | AZ769838 1M0570H22 |
| 35 | 8.8 | 58.7 | 22 | 8 | AZ603366 | AZ603366 1M0422L17 |
| C 36 | 8.8 | 58.7 | 23 | 8 | AZ762598 | AZ762598 1M0557I12 |
| 37 | 8.8 | 58.7 | 23 | 8 | AZ844618 | AZ844618 2M0144M03 |
| C 38 | 8.8 | 58.7 | 24 | 8 | AZ514503 | AZ514503 1M0361J19 |
| C 39 | 8.8 | 58.7 | 24 | 9 | AG201951 | AG201951 Pan trogl |
| C 40 | 8.8 | 58.7 | 24 | 9 | TA181A05Q | TA181A05Q T. brucei |
| 41 | 8.8 | 58.7 | 25 | 1 | AI720628 | AI720628 as70g12.x |
| C 42 | 8.8 | 58.7 | 25 | 9 | TA283B04P | TA283B04P T. brucei |
| C 43 | 8.8 | 58.7 | 26 | 8 | AZ654939 | AZ654939 1M0529N04 |
| C 44 | 8.8 | 58.7 | 26 | 8 | AZ771925 | AZ771925 1M0574P19 |
| C 45 | 8.8 | 58.7 | 26 | 8 | AZ941927 | AZ941927 2M0201D24 |

ALIGNMENTS

RESULT 1
L32033/c
LOCUS HUMXP11B6B Human placenta Homo sapiens cDNA clone XP11B6B, mRNA
DEFINITION sequence.
ACCESSION L32033
VERSION L32033.1 GI:927075
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lee, C.-C., Yazdani, A., Wehnert, M., Bailey, J., Couch, L., Xiong, M., Coolbaugh, M.I., Chinault, C.A., Baldini, A., Lindsay, E.A., Zhao, Z.-Y. and Caskey, C.T.H.
TITLE Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries
JOURNAL Hum. Mol. Genet. 4, 1373-1380 (1995)
MEDLINE 95090257
PubMed 7581376
COMMENT Contact: Caskey, C.T.H.
FEATURES
Location/Qualifiers
source
1..24
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="Xp11.2"
/clone="XP11B6B"
/notes="Human placenta"
/note="Arrayed cDNAs and cosmid libraries from human placental tissue"

ORIGIN

Query Match 72.0%; Score 10.8; DB 7; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.1e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AGATACCACACGCA 14
||| ||||| |||||
Db 19 AGAAACCAACAGGCA 6

RESULT 2

AZ794953
LOCUS AZ794953
DEFINITION 2M0048N21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
24 bp DNA linear GSS 16-FEB-2001

clone UUGC2M0048N21 R, genomic survey sequence.

```

ACCESSION      A2794953
VERSION        A2794953.1  GI:12941458
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

REFERENCE
AUTHORS        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
               Ielam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
               Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
               Niederhausern, A., and Wright, D., Weiss, R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0048 row: N column: 21
               Seq primer: CACACGAGAACACTATGACC
               Class: plasmid ends
               High quality sequence stop: 24.
FEATURES       source
               1..24
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC2M0048N21"
               /sex="Male"
               /lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UGCLM library"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptored DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptored mouse DNA was annealed to
               adaptored vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
ORIGIN
Query Match      69.3%; Score 10.4; DB 8; Length 24;
Best Local Similarity 91.7%; Pred. No. 3.5e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AGATACCACACG 12
       ||| |||||
Db      1 AGAGACCACACG 12

RESULT 3
LOCUS      BH792752
DEFINITION SALK_064997.35.25.x Arabidopsis thaliana TDNA insertion lines
               26 bp DNA linear GSS 02-APR-2002

REFERENCE
AUTHORS        Bh792752
TITLE          SALK_064997.35.25.x Arabidopsis thaliana TDNA insertion lines
               26 bp DNA linear GSS 02-APR-2002
JOURNAL        Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE        22755829
PUBMED         12874060

```

```

Arabidopsis thaliana genomic clone SALK_064997.35.25.x, genomic
survey sequence.
BH792752      BH792752.1  GI:19889882
KEYWORDS       GSS.
SOURCE         Arabidopsis thaliana (thale cress)
ORGANISM       Arabidopsis thaliana

REFERENCE
AUTHORS        Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
               Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
               Shinn, P., Zimmerman, J., and Ecker, J.R.
TITLE          A Sequence-indexed Library of Insertion Mutations in the
               Arabidopsis Genome
JOURNAL        Unpublished (2001)
COMMENT        Contact: Joseph R. Ecker
               Salk Institute Genomic Analysis Laboratory (SIGNAL)
               The Salk Institute for Biological Studies
               10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
               Tel: 858 453 4100 x1752
               Fax: 858 558 6379
               Email: ecker@salk.edu
               This is single pass sequence recovered from the left border of
               TDNA.
FEATURES       Class: TDNA tagged.
               Location/Qualifiers
               1..26
               /organism="Arabidopsis thaliana"
               /mol_type="genomic DNA"
               /ecotype="Col-0"
               /db_xref="taxon:3702"
               /clone="SALK_064997.35.25.x"
               /clone_lib="Arabidopsis thaliana TDNA insertion lines"
               /note="PCR was performed on Arabidopsis thaliana lines
               each of which contains one or more TDNA insertion
               elements. The resultant fragment for each line was
               directly sequenced to determine the genomic sequence at
               the site of insertion. Details of the protocols used can
               be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match      69.3%; Score 10.4; DB 8; Length 26;
Best Local Similarity 91.7%; Pred. No. 3.5e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AGATACCACACG 12
       ||| |||||
Db      8 AGATTCACACG 19

RESULT 4
LOCUS      BX896975
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-764A02-024030,
               genomic survey sequence.
ACCESSION      BX896975
VERSION        BX896975.1  GI:39929470
KEYWORDS       GSS.
SOURCE         Arabidopsis thaliana (thale cress)
ORGANISM       Arabidopsis thaliana

REFERENCE
AUTHORS        Li, Y., Rosso, M.G., Strizhov, N., Vishnover, P. and Weissshaar, B.
TITLE          GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
               the identification of T-DNA insertion mutants in Arabidopsis
               thaliana
JOURNAL        Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE        22755829
PUBMED         12874060

```

2 Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weishaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL MEDLINE PUBLISHED 23117147
REFERENCE 14756321

3 Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weishaar,B.
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
BioTechniques 35 (6), 1164-1168 (2003)
JOURNAL PUBLISHED 14682050
REFERENCE 1 (bases 1 to 30)

4 Rosso,M.G., Strizhov,N., Li,Y. and Weishaar,B.
Direct Submission
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At1g03300.
Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
Location/Qualifiers
1. 30
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-76402-024030"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pGAB1 (GenBank accession number: AY529716). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 69.3%; Score 10.4; DB 9; Length 30;
Best Local Similarity 91.7%; Pred. NO. 3.6e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGATACACACG 12
| | | | | | | | | |
Db 15 AGATACACACAG 26

RESULT 5
AZ782314/c
LOCUS
DEFINITION 2M0022D03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0022D03 R, genomic survey sequence.
ACCESSION AZ782314
VERSION AZ782314.1 GI:12915912
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL COMMENT
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0022 row: D column: 03
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0022D03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 66.7%; Score 10; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. NO. 5.9e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCACACGACG 15
| | | | | | | | | |
Db 15 CCACACGACG 6

RESULT 6
TA205F05Q
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 205f05, reverse sequence, genomic survey sequence.
ACCESSION AL476402
VERSION AL476402.1 GI:11843069
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
1 (bases 1 to 22)
REFERENCE
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Barrell, nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

```
1. .23
  /organism="Trypanosoma brucei"
  /mol_type="genomic DNA"
  /strain="TREU927"
  /db_xref="taxon:5691"
  /clones="205f05"
```

ORIGIN

Query Match 66.7%; Score 10; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ACCACACGCA 14

|||||
Db 13 ACCACACGCA 22

RESULT 7

TA313C04P

LOCUS

DEFINITION T. brucei sheared genomic DNA clone 313c04, forward sequence, genomic survey sequence.

ACCESSION

AL490295

VERSION

AL490295.1

KEYWORDS

GSS.

SOURCE

Trypanosoma brucei

ORGANISM

Trypanosoma brucei

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Constructured at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Barrell, nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

```
1. .23
  /organism="Trypanosoma brucei"
  /mol_type="genomic DNA"
  /strain="TREU927"
  /db_xref="taxon:5691"
  /clones="313c04"
```

ORIGIN

Query Match 66.7%; Score 10; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GATACCACAC 11

|||||
Db 2 GATACCACAC 11

RESULT 8

AI664044/c

LOCUS

DEFINITION

ue73805.r1 Soares NMPu Mus musculus cDNA clone IMAGE:1496768 5' similar to SW:CHHC_BOMMO P20730 CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR ; mRNA sequence.

ACCESSION

AI664044

VERSION

AI664044.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LML ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:934372

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.

FEATURES

source

```
1. .25
  /organism="Mus musculus"
  /mol_type="mRNA"
  /db_xref="taxon:10090"
  /clone="IMAGE:1496768"
  /sex="female"
  /dev_stage="adult"
  /lab_host="DH10B"
  /clone_lib="Soares NMPu"
  /notes="Organ: uterus; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
```

ORIGIN

Query Match 66.7%; Score 10; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ACCACACGCA 14

|||||
Db 25 ACCACACGCA 16

RESULT 9

AZ770749/c

LOCUS

DEFINITION

1M0572B01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0572B01 R, genomic survey sequence.

ACCESSION

AZ770749

```

VERSION      AZ770749.1  GI:12892278
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D. Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0572 row: B column: 01
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
                1..20
                  /organism="Mus musculus"
                  /mol_type="genomic DNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="UUGC1M0572B01"
                  /sex="Male"
                  /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                  /notes="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained from the Jackson
                  Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/). The DNA
                  was hydrodynamically sheared by repeated passage through a
                  0.005 inch orifice at constant velocity. The sheared DNA
                  was blunt end-repaired with T4 DNA polymerase and T4
                  polynucleotide kinase. Adaptor oligonucleotides were
                  ligated to the blunt ends in high molar excess. The
                  adaptor DNA was purified and size-selected for a 9.5 to
                  10.5 kb range using preparative agarose gel
                  electrophoresis. Vector DNA was prepared from a derivative
                  of pWD42 (G14732114|gb|AF129072.1), a copy-number
                  inducible derivative of plasmid R1. The vector was ligated
                  with adaptors complementary to the insert adaptors and
                  purified. The sheared, adaptor mouse DNA was annealed to
                  adaptor vector DNA, and transformed into
                  chemically-competent E. coli XL10-Gold (Stratagene) cells
                  and selected for ampicillin resistance."

ORIGIN
Query Match      65.3%; Score 9.8; DB 8; Length 20;
Best Local Similarity 84.6%; Pred. No. 7.7e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATACCACAGCAG 15
   |||||
Db 13 ACACCAAGCAG 1

RESULT 10
AZ307506
LOCUS
DEFINITION
clone UUGC1M0009116 F, genomic survey sequence.
ACCESSION
AZ307506

```

```

VERSION      AZ307506.1  GI:10346574
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D. Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0009 row: I column: 16
              Seq primer: CGTTGTAACACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
                1..20
                  /organism="Mus musculus"
                  /mol_type="genomic DNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="UUGC1M0009116"
                  /sex="Male"
                  /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                  /notes="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained from the Jackson
                  Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/). The DNA
                  was hydrodynamically sheared by repeated passage through a
                  0.005 inch orifice at constant velocity. The sheared DNA
                  was blunt end-repaired with T4 DNA polymerase and T4
                  polynucleotide kinase. Adaptor oligonucleotides were
                  ligated to the blunt ends in high molar excess. The
                  adaptor DNA was purified and size-selected for a 9.5 to
                  10.5 kb range using preparative agarose gel
                  electrophoresis. Vector DNA was prepared from a derivative
                  of pWD42 (G14732114|gb|AF129072.1), a copy-number
                  inducible derivative of plasmid R1. The vector was ligated
                  with adaptors complementary to the insert adaptors and
                  purified. The sheared, adaptor mouse DNA was annealed to
                  adaptor vector DNA, and transformed into
                  chemically-competent E. coli XL10-Gold (Stratagene) cells
                  and selected for ampicillin resistance."

ORIGIN
Query Match      62.7%; Score 9.4; DB 8; Length 20;
Best Local Similarity 90.9%; Pred. No. 1.3e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACCACAGCAG 15
   |||||
Db 9 ACCACACAG 19

RESULT 11
AZ346725
LOCUS
DEFINITION
clone UUGC1M0082P06 F, genomic survey sequence.
ACCESSION
AZ346725

```

A2346725.1 GI:10425962
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: P column: 06
Seq primer: CGTTGTAACAGCAGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0082P06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 62.7%; Score 9.4; DB 8; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGATACCACAC 11
||| |||||
Db 8 AGACACCAC 18

RESULT 12
AI613292
LOCUS
DEFINITION
ty35902.x1 NCI_CGAP Ut2 Homo sapiens cDNA clone IMAGE:2281106.3,
similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST ; contains element
MSR1 repetitive element ; mRNA sequence.

JOURNAL
Unpublished (2000)
parasitoid insects.

JOURNAL
Unpublished (2000)
parasitoid insects.

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0017 row: P column: 15
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

source

1. .22
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0017P15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 61.3%; Score 9.2; DB 8; Length 22;
Best Local Similarity 78.6%; Pred. No. 1.7e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GATACCAACGACGAG 15

Db 20 GGTATCATGTCAG 7

Search completed: June 23, 2005, 19:42:35
Job time : 2986 secs